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Regulatory Characteristics of Bacillus pumilus Protease Promoters

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Abstract

© 2017, Springer Science+Business Media New York.Expression of extracellular protease genes of Bacilli is subject to regulation by many positive and negative regulators. Here we analyzed 5′ regulatory regions of genes encoding proteolytic proteases AprBp, GseBp, and MprBp from Bacillus pumilus strain 3–19. Gfp fusion constructs with upstream genomic regions of different lengths were created for all three genes to identify their natural promoters (regulatory regions). Our results suggest that the aprBp gene, encoding the major subtilisin-like protease, has the most extensive promoter region of approximately 445 bp, while the minor protease genes encoding glutamyl endopeptidase (gseBp) and metalloproteinase (mprBp) are preceded by promoters of 150 and 250 bp in length, respectively. Promoter analysis of PaprBp-gfpmu3 and PgseBp-gfpmu3 reporter fusion constructs in degU and spo0A mutants indicates a positive regulatory effect of DegU and Spo0A on protease expression, while the disruption of abrB, sinR, and scoC repressor genes did not significantly affect promoter activities of all protease genes. On the other hand, the expression of PaprBp-gfpmu3 and PgseBp-gfpmu3 reporters increased 1.6- and 3.0-fold, respectively, in sigD-deficient cells, indicating that the prevention of motility gene expression promotes protease expression. Our results indicate that all examined regulators regulated serine proteases production in B. subtilis.

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